

Automatic Segmentation of Thalamic Nuclei with STEPS Label Fusion

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Target Audience: Scientists interested in automatic segmentation of the thalamus and its nuclei, esp. for the study of atrophy or treatment targeting.

Purpose: The white matter nulled MPRAGE (WMnMPRAGE) contrast at 7T has recently enabled detailed delineation of thalamic nuclei guided by the Morel atlas, but this demanded tedious manual segmentation by a trained neuroradiologist.^{1,2} Unfortunately, such a manual procedure is difficult to scale to larger studies and applications. We present the development of a semi-automated thalamic segmentation method, leveraging the manual thalamic segmentations accomplished to date via label fusion and nonlinear registration to a study-specific template. Similar schemes have proven successful in subcortical structures such as the hippocampus, brain stem, caudate, and putamen.^{1,3,4}

Methods: After informed consent, a study group of 12 multiple sclerosis patients and 6 controls were scanned on a 7T scanner (Discovery MR950, GE Healthcare) using a 32 channel head coil (Nova Medical). WMnMPRAGE scan parameters: TI 680ms, 180x180x200 matrix, slice thickness 1mm, FOV 18cm, flip angle 4°, TS 6s, BW 12 kHz, TR 10ms, ARC parallel imaging 1.5x1.5 (2D radial fanbeam). Scan times were 5 minutes. Previously, a separate atlas group of 6 controls were acquired with an unaccelerated, 1D-centric-ordered version of the WMnMPRAGE protocol (16 min). The whole thalami and 15 thalamic nuclei of these controls were manually delineated with a high degree of reproducibility.¹ In this study, we chose the 12 more well-delineated nuclei from these atlas controls to create the thalamic atlas, which was used to guide the segmentation of a new subject. First, a WMnMPRAGE mean brain template was created from 17 out of 18 subjects in the study group. One randomly chosen target patient was left out as our test case so that the template remained unbiased. ANTS was used with its default parameters to create the template.⁵ The resulting mean brain encompasses both normal and diseased brain states, making it more suitable for registration of atrophied brains. Next, the 6 controls of the atlas group were registered to this template and the atlas for each thalamic structure was formed by warping the manual delineations to this space with nearest-neighbor interpolation. Similarly, the target patient was registered to the template. Label fusion by the STEPS algorithm of Cardoso et al.⁶ was then performed using NiftySeg with a kernel size of 5 voxels and Markov random field smoothing of $\beta=3$. STEPS uses knowledge of the local voxel-wise registration accuracy to inform its decision of how to combine the candidate segmentations from the thalamic atlas. These parameters were determined independently using one of the atlas controls as a training set. Finally, each of the automatically-derived segmentations was warped back into the target's native space with nearest neighbor interpolation. They were then compared against manually delineated truth labels of the target patient using Dice's coefficient.

Results: A total of 16 iterations were required for ANTS to converge to a mean template. This took over 6 days on a 12-core 2.66 GHz Intel Xeon. The template shows a remarkable amount of detail due to its 1mm resolution and the WMnMPRAGE contrast (Fig. 1). We also attempted to create an alternate template with the more conventional CSF-nulled MPRAGE images. Surprisingly, this converged more slowly with much less progress made after 4 iterations compared to the WM-nulled variant. Fig. 2 shows the results of the automatic segmentation with STEPS, where the truth is outlined in yellow and the algorithm is the filled in colored region. Table 1 displays the Dice coefficient performance for each of the regions of interest. In particular, the predictions for whole thalamus (0.87), pulvinar nucleus (Pul, 0.77), mediodorsal nucleus (MD, 0.71), and center median nucleus (CM, 0.71) were quite accurate. This is comparable to existing multi-modal methods that require more complex acquisitions including DTI.⁷

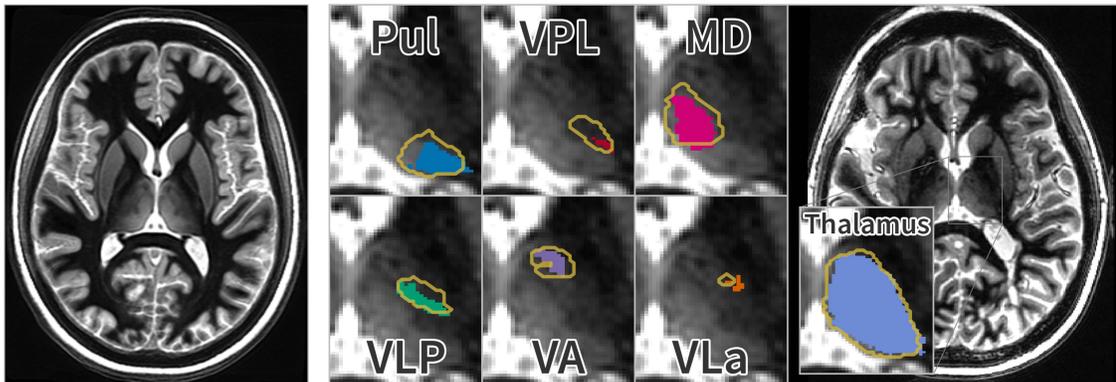


Fig. 1: An axial slice from the 1mm resolution WMnMPRAGE template of 17 subjects at 7T.

Fig. 2: Automatic segmentations (filled region) for whole thalamus and nuclei with the manual truth (yellow outline) overlaid in the target patient. The predicted label is typically underestimated. See [1] for the abbreviation glossary.

	Dice	Median Dice in [7]
Whole Thalamus	0.870	N/A
AV	0.524	N/A
VA	0.496	N/A
Vla	0.495	N/A
VLP	0.571	N/A
VPL	0.458	N/A
Pul	0.774	0.725
LGN	0.473	0.405
MGN	0.610	0.515
CM	0.709	N/A
MD	0.709	N/A
Hb	0.584	N/A
MTT	0.251	N/A

Table 1: Performance of the algorithm compared to a previous multi-modal technique.

Discussion/Conclusion: We demonstrate that label fusion with registration to a WMnMPRAGE template provides an effective means to achieve automatic whole thalamus segmentation, as well as a good starting point for most nuclei with a single image acquisition. Performance can be improved upon with a greater number of manual priors; 15 subjects has been suggested as optimal for STEPS while we have only used 6 in our atlas group.⁶ In general, the automatic segmentations appear to be underestimating the structures. Machine learning techniques like adaptive boosting, perhaps with information supplied by quantitative mapping, may help correct such systematic biases as in [3]. Reliable automatic segmentation of the thalamus and its nuclei is vital for any large scale study of thalamic atrophy with disease. It also has significant applications in treatment planning where there is a critical need for better localization of specific nuclei for targeting. The work presented here is a substantial step toward this goal; it is also worth noting that we are tackling the more difficult problem of segmenting diseased brains based on normal priors.

References: [1]Tourdias et al. Neuroimage. 2013 Sep 7;84C:534-545 [2]Niemann et al. Neuroimage. 2000 Dec;12(6):601-16. [3]Yushkevich et al. Neuroimage. 2010 Dec;53(4):1208-24. [4] Babalola et al. Neuroimage. 2009 Oct 1;47(4):1435-47. [5]Avants et al. Med Image Anal. 2008 Feb;12(1):26-41. [6]Cardoso et al. Med Image Anal. 2013 Aug;17(6):671-84. [7]Stough et al. Proc IEEE Int Symp Biomed Imaging. 2013:852-855.

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